

Application No.: 09/508,79**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

## SEQUENCE LISTING

&lt;110&gt; Miyata, Toshio

&lt;120&gt; MEGSIN PROTEIN

&lt;130&gt; SHIM004

&lt;140&gt; 09/508,997

&lt;141&gt; 2000-06-27

&lt;150&gt; PCT/JP98/04269

&lt;151&gt; 1998-09-22

&lt;150&gt; 9/275302

&lt;151&gt; 1997-09-22

&lt;160&gt; 44

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1867

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; n is an unknown and may be any natural amino acid

&lt;400&gt; 1

atggcctccc ttgctgcagc aaatgcagag ttttgcttca acctgttcmt aasruaaaaa 60  
aasnaaguhc yshasnuhag agagatggat gacaatcaag gaaatggaaa tgtgttcttt 120  
tcctctargg umtasasasn gngyasngya snvahhsrsr ctgagcctct tcgctgcctt 180  
ggccctgggc cgcttgggag ctcaagatus ruhaaaauaa uvaargugya agnasgactc 240  
cctctctcag attgataagt tgcttcatgt taacactgcc tcaassrusr gnasysuhs 300  
vaasnthraa srggatattg aaactcttct aatagtcagt cagggtctca gtctcaactg 360  
gytyrgyasn srsrasnrg nsrgyugnsr gnuaaaagag tttttctga tataaatgca 420  
tcccacaagg attatgatct cysargvahn rasasnaasr hsysastyra suagcattgt 480  
gaatgggctt ttgctgaaa aagtgtatgg ctttcataag srvaasngyu haaguysvat 540  
yrgyhhsysg actacattga gtgtgccgaa aaattatacg atgccaaagt ggagcgaast 600  
yrgucysaag uysutyraa aysvaguarg gttgacttta cgaatcattt agaagacact 660  
agacgtaata ttaataagva ashthrasnh suguasthra rgargasnas nystgggttg 720  
aaaatgaaac acatggcaaa atcaagaacg tgattgggtga atrvaguasn guthrhsgyy 780  
sysasnvyg guggtggtcat aagctcatct gctgtaattg tgctggtgaa tgctgtgtac 840  
gygysrsr aavamivauv aasnaavaty rtcaaaggc aagtggaat cagccttcac 900  
caagagcgaa accataaath ysgystrgn sraathrys srguthrasn tgccatttca 960  
aatctcccaa gtgctctggg aaggcagtcg ccatgatgcy shshyssrry scyssrgyys 1020  
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ngnuargysh asnusrvagu asrsrmtaag attcttgagc tcagatacaa tgggtggcata 1140  
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ctctctgaaa ttgaaaacaa actgacctt cagurguasn asusrgugua snysuthrhg 1260  
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hrasnrga rgmthrsry styrvagagg tatttttcc tcagtccaag atagagaaga 1380

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 agatctctct gggattgctt cgggggggtcg tctgtatata tcaaggaaas usrgyaasrg 1560  
 ygyargutyr srargatgat gcacaaatct tacatagagg tcaactgagga gggcaccgag 1620  
 gctmtmthsy ssrtyrguva thrugugyt hrguaaactg ctgccacagg aagtaatatt 1680  
 gtagaaaagc aactccctca gtcccthrraa athrgysras nvaguysgnu rgnsracgct 1740  
 gtttagagct gaccacccat tctatttgt tatcaggaag gatthruhar gaaashsrhu 1800  
 hvaargysas gacatcatct tattcagtgg caaagtttct tgccttgaa suhsrgyysv 1860  
 asrcysr 1867

&lt;210&gt; 2

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe  
 1 5 10 15  
 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser  
 20 25 30  
 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp  
 35 40 45  
 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser  
 50 55 60  
 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu  
 65 70 75 80  
 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu  
 85 90 95  
 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys  
 100 105 110  
 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg  
 115 120 125  
 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys  
 130 135 140  
 Trp Val Glu Asn Gly Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu  
 145 150 155 160  
 Gly Gly Ile Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165 170 175  
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn  
 180 185 190  
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met  
 195 200 205  
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met  
 210 215 220  
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu  
 225 230 235 240  
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln  
 245 250 255  
 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val  
 260 265 270  
 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys  
 275 280 285  
 Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys  
 290 295 300  
 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

- 3 -

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Rattus rattus

&lt;220&gt;

&lt;223&gt; Xaa indicates a naturally occurring unknown amino acid

&lt;400&gt; 4

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe

1 5 10 15

Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20 25 30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35 40 45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser

50 55 60

Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu

65 70 75 80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu

85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys

100 105 110

Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg

115 120 125

Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys

130 135 140

Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp

145 150 155 160

Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr

165 170 175

Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser

180 185 190

Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met

195 200 205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met

210 215 220

Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met

225 230 235 240

Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln

245 250 255

Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val

260 265 270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg

275 280 285

Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg

290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys

305 310 315 320

Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala

325 330 335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser

340 345 350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn

355 360 365

Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 370 375 380

&lt;210&gt; 5

&lt;211&gt; 1848

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;223&gt; n is an unknown and may be any natural amino acid

&lt;400&gt; 5

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 tccgtctghh srsrusrth raauthruar guggtgctcg aggtgactgt gcacgtcaga 180  
 ttgacaaggc actgcacttt gyaaarggya scysaaargg nasysaauhs haacatacca 240  
 tcaagacaag gaaactcatc taataatcag ccaggactta snrsrarggn gyasnsrsra 300  
 snasngnrgy ucagtatcaa ttgaaaagag ttcttgctga cataaactca tctcataagg 360  
 ntyrgnuysa rgvauaaasa snrsrshys gattatgaac tcagcattgc cactggagtt 420  
 ttgcagaaa aagtctatas tyrguusraa thrgyvaha guysvatyrg actttcataa 480  
 gaactacatt gagtgtgctg aaaacttata caatgctash hsysasntyr gucysaagua 540  
 snutyraasna aaaagtgga agagttgact tcacaaatga tgtacaagat accagattty 600  
 svaguargva ashthrasna svagnasthr arghaaaatt aataaatgga ttgaaaatga 660  
 gacacatgga aagatcaaga agysasnyst rguasnguth rhsgyysysy sgtgttgggc 720  
 gacagcagcc tcagctcgtc ggctgtcatg gtgctggtgv augyassrsr usrsrsraav 780  
 amtvaauvaa cgctgtttac ttcaaaggca aatggaaatc ggccttcacc aagactasna 840  
 avatyryhsg yystryssra ahthrysthr gataccctca gttgccgttt taggtctccc 900  
 acgtgtcctg gaaaagtaas thrusrcysa rghargsrr hrcysrgyys vagttaatat 960  
 gatgcataca gaacggcggt tcaattgtc taccattcag vaasnmtmth sgnguargar 1020  
 ghasnusrth rgncagccac caatgcaggt tcttgagctc caatatcatg gtggcataag 1080  
 cgnrrmtgnv auguugntyr hsgygysrat gtacattatg ctgcctgagg atggcctatg 1140  
 tgaaattgaa agcaagmtty rmturguasg yucysgugus rysctgagtt tccagaatct 1200  
 gatggactgg accaatagga ggaaaatgaa ausrhgnasn umtastrthr asnargargy 1260  
 smtystctca gtatgtgaac gtgtttctcc ccagttcaa gatagagaag aatsrgntyr 1320  
 vaasnvhur gnhyguysa sntatgaaat gacgcaccac ttgaaatcct taggcttgaa 1380  
 agatatcttt tyrgumtthr hshsuyssru gyuysashga tgagtcaggt gcagatctct 1440  
 ctggaattgc ctctggaggt cgtctcasgu srsraaasus rgyaasrgyg yargutacgt 1500  
 atcaaagcta atgcacaagt cattcataga ggtctcagag gagtyrvasr ysumthsyss 1560  
 rhguvasrgu guggcactga agccactgct gccacagaaa ataacattgt tgaaaagcag 1620  
 gythrguaat hraaaathrg uasnasnvag uysgncttcc tgagtccaca gtgttcagag 1680  
 ccgaccgccc ctttctgttt gtcurgusrt hrvahargaa asargrhuhv aatcaagaag 1740  
 aatgacatca tcttatttac tggcaaagtc tctgtctcty sysasnasuh thrgyysvas 1800  
 rcysrtgaaa ttcgatttgg ttctctatac agtaacaggc atcaagaa 1848

&lt;210&gt; 6

&lt;211&gt; 368

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 6

Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val

1

5

10

15

Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu

20

25

30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe  
 35 40 45  
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
 50 55 60  
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
 65 70 75 80  
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
 85 90 95  
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala  
 100 105 110  
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe  
 115 120 125  
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys  
 130 135 140  
 Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val  
 145 150 155 160  
 Asn Ala Val Tyr Phe Lys Lys Trp Lys Ser Ala Phe Thr Lys Thr  
 165 170 175  
 Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val  
 180 185 190  
 Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln  
 195 200 205  
 Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser  
 210 215 220  
 Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys  
 225 230 235 240  
 Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys  
 245 250 255  
 Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn  
 260 265 270  
 Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe  
 275 280 285  
 Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu  
 290 295 300  
 Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu  
 305 310 315 320  
 Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln  
 325 330 335  
 Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val  
 340 345 350  
 Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 355 360 365

&lt;210&gt; 7

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthesis

&lt;400&gt; 7

tgtaaaacga cggccagt

18

<210> 8  
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<220>  
<223> Synthesis

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<210> 9  
<211> 15  
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<213> Artificial Sequence

<220>  
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<400> 9  
tcagagaggt cattc 15

<210> 10  
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<212> DNA  
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<220>  
<223> Synthesis

<400> 10  
tcattgatgg gtcctcaa 18

<210> 11  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesis

<400> 11  
agattcttga gctcagat 18

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesis

<400> 12  
aatggtggca taaacatg 18



<210> 13  
<211> 18  
<212> DNA  
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<220>  
<223> Synthesis

<400> 13  
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<210> 14  
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<210> 15  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 17  
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<210> 18  
<211> 15  
<212> PRT  
<213> Artificial Sequence

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<223> Synthesis

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Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg  
1 5 10 15

<210> 19  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesis

<400> 19  
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1 5 10 15

<210> 20  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesis

<400> 20  
Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp  
1 5 10 15

<210> 21  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthesis

<400> 21  
Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu  
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<210> 22  
<211> 38  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 22

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<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

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<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> n is an unknown and may be any natural amino acid

<400> 24

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<210> 25

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

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<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> n is an unknown and may be any natural amino acid

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<210> 27

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 27

cgacctccag aggcaattcc agagagatca gccctgg

37

<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 28

gtctccaag cctacagatt tcaagtggt cctc

34

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 29

gctcaggga gtgaagatgc tcagggaaga

30

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 30

ctgacgtgca cagtcacctc gagcacc

27

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 31

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<210> 32

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 32

ctctatagga gacacttg

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<210> 33

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 33

gaaacaaatc aaagcaaac

19

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 34

gaaattgaaa rcaarctgas yttycagaat

30

<210> 35

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 35

ctgasyttc agaataat ggamtgac

29

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 36

ggaytsaggr agtwgctttt cwacratrtt

30

<210> 37

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 37

gaggtctcag aggagggcac tgaagccact gctgcc

36

<210> 38

<211> 39

<212> DNA

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<220>

<223> Synthesis

<400> 38

ccagtcgaga tctctctgga attgcctctg gaggtcgtc

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<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 39

gcctgttact gtataggaaa ccaaaccg

28

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 40

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<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 41

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24

<210> 42

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 42

ataagcttc atcatcaagg gcaag

25

<210> 43

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 43

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44

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 44

tatcctgagg cagtgttaac aagcaac

27

**Bozicevic, Field & Francis LLP**  
**200 Middlefield Road, Suite 200**  
**Menlo Park, California 94025**  
**(650) 327-3400**

**Applicant(s): Toshio Miyata**

**Title: Megsin Protein**

**Filing Date: June 27, 2000**

**Serial No.: 09/508,997**

**Attorney Docket No.: SHIM004**